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DLAPRG US LLP

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Inventors: Lori CLARKE, et al. for NOVEL VECTOR CONSTRUCTS


Attorney: Linda R. Judge, 415-836-2586;


Atty. Docket: 3802-162-27

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A. CTTATCGATACCGTCGAAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCAT
CACAAATTTACAAATAAAGCATTTTTTCTACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCA
+++++ ↑ ++++++
ATGTATCTTATCATGTC CLEAVAGE SITE

B.  AAUAAA
+++++ GCA

C.  GCAaaaaaaaaaaaaaaaaaaaaaaaaa

+ UPSTREAM AND DOWNSTREAM
CLEAVAGE-POLYADENYLATION ELEMENTS

Fig. 1

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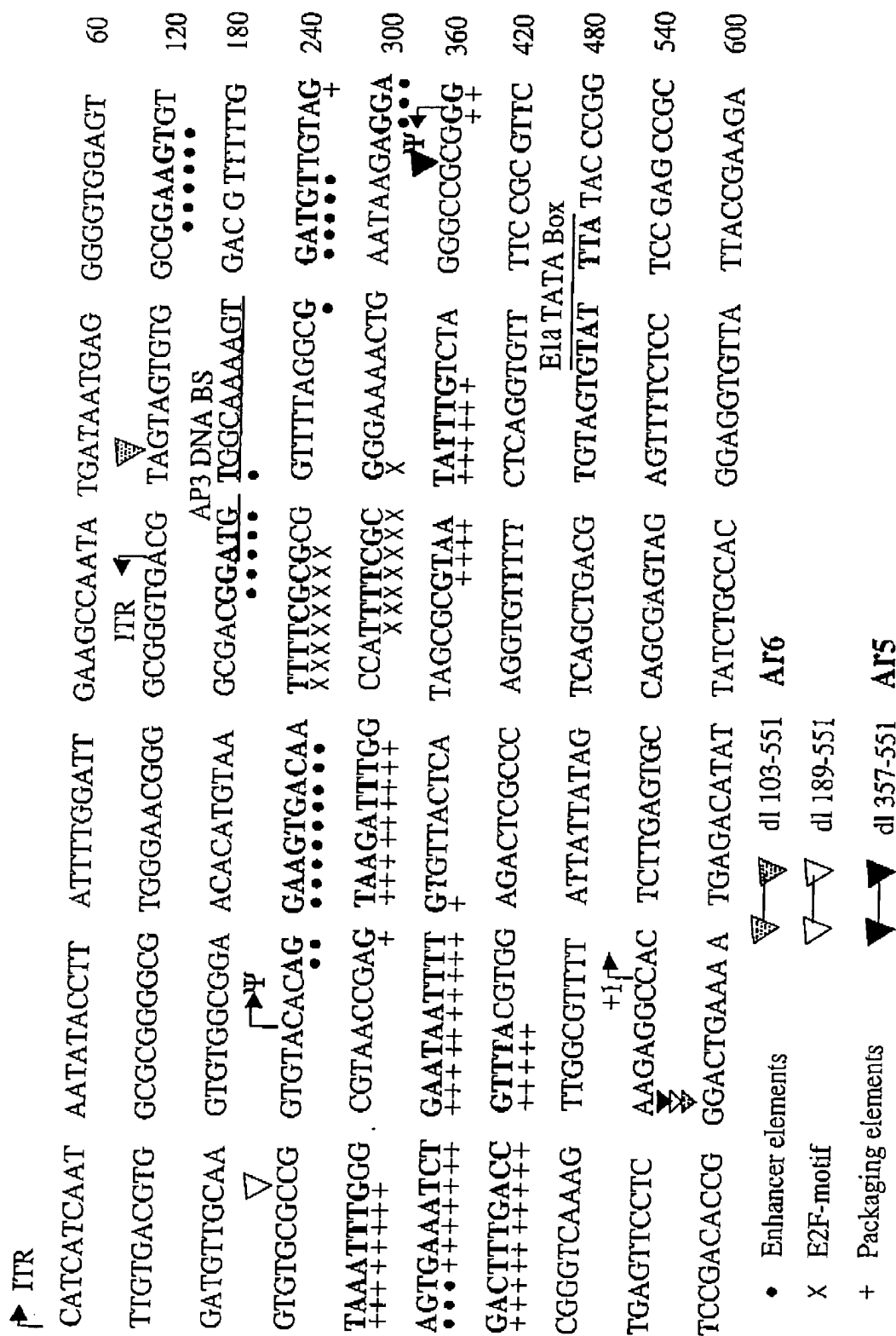


Fig. 2

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1 CATCATCAATAATATACCTTATTTTGGATTGAAGCCAATATGATAATGAGGGGGTGGAGT
+-----ITR-----+
61 TTGTGACGTGGCGCGGGCGGTGGGAACGGGGCGGGTGACGTAGGGCGCGATCAAGCTTAT
+-----ITR-----+
121 CGATACCGTCGAAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATC
-----polyA-----
181 ACAAATTTACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTC
-----polyA-----
241 ATCAATGTATCTTATCATGTCTGGATCCGCGCCGCTAGCGATCATCCGACAAAGCCTGC
-----+-----+
301 GCGCGCCCCGCCCCGCCATTGGCCGTACCGCCCCGCGCCGCGCCCATCTCGCCCCCTCG
-----E2F-1 PROMOTER-----
361 CCGCCGGGTCCGGCGCGTTAAAGCCAATAGGAACCGCCGCGGTTGTTCCCGTCACGGCCG
-----E2F-1 PROMOTER-----
421 GGGCAGCCAATTGTGGCGGCGCTCGGCGGCTCGTGGCTCTTTCGCGGCAAAAAGGATTTG
-----E2f-1 PROMOTER-----
481 GCGCGTAAAAGTGGCCGGGACTTTGCAGGCAGCGGCGGCGGGGGCGGAGCGGGATCGAG
-----E2f-1 PROMOTER-----
541 CCTTCGATGATATCAGATCATCGGATCCCGGTGCGACTGAAAATGAGACATATTATCTGCC
-----+-----+
601 ACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTGGACCAGCTGATCGAAGAGG
-----E1a GENE-----
661 TACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCACCTACCTTCACGAAGTGT
-----E1a GENE-----
721 ATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGAGGAGGCGGTTTCGCAGATTTTTC
-----E1a GENE-----
781 CCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTACTCACTTTTCCGCCGGCGC
-----E1a GENE-----
841 CCGGTTCTCCGGAGCCGCCTCACCTTTCCCGGCAGCCCGAGCAGCCGGAGCAGAGAGCCT
-----E1a GENE-----

Fig. 3A

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901 TGGGTCCGGTTTCTATGCCAAACCTTGTACCGAGGTGATCGATCTTACCTGCCACGAGG
-----E1a GENE-----

961 CTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGTGAGGAGTTTGTGTTAGATTATG
-----E1a GENE-----

1021 TGGAGCACCCCGGGCACGGTTGCAGGTCTTGTATTATCACCGGAGGAATACGGGGGACC
-----E1a GENE-----

1081 CAGATATTATGTGTTTCGCTTTGCTATATGAGGACCTGTGGCATGTTTGTCTACAGTAAGT
-----E1a GENE-----

1141 GAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTGGTGTGGTAATTTTTTTTAAAT
-----E1a GENE-----

1201 TTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGATTTTTTTAAAGGTCCGTGTGTC
-----E1a GENE-----

1261 TGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAAGACCTACCCGCCGTCTCTAA
-----E1a GENE-----

1321 AATGGCGCCTGCTATCCTGAGACGCCCCGACATCACCTGTGTCTAGAGAATGCAATAGTAG
-----E1a GENE-----

1381 TACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTGAGATACACCCGGTGGTCCC
-----E1a GENE-----

1441 GCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGCGTCGCCAGGCTGTGGAATG
-----E1a GENE-----

1501 TATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACTTGAGCTGTAAACGCCCCAG
-----E1a GENE-----

1561 GCCATAAGGTGTAAACCTGTGATTGCGTGTGTGGTTAACGCCTTTGTTTGCTGAATGAGT
-----E1a GENE-----

1621 TGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACTTGCATGGCGTGTAAATGGGGC
-----E1a GENE-----

1681 GGGGCTTAAAGGGTATATAATGCGCCGTGGGCTAATCTTGGTTACATCTGACCTCATGGA
-----E1b GENE-----

1741 GGCTTGGGAGTGTTTGAAGATTTTTCTGCTGTGCGTAACTTGCTGGAACAGAGCTCTAA
-----E1b GENE-----

1801 CA

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Fig. 3B

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33881 AACCTACGCCCAGAAACGAAAGCCAAAAACCCACAACCTTCCTCAAATCGTCACTTCCGT
33941 TTTCCACGTTACGTCACTTCCCATTTTAATTAAGAATTCTACAATTCCCAACACATACA
34001 AGTTACTCCGCCCTAAAACCCCTGGGCGAGTCTCCACGTAAACGGTCAAAGTCCCGCGGC
+ PACKAGING SIGNAL-----
34061 CCTAGACAAATATTACGCGTATGAGTAACACAAAATTATTCAGATTTCACTTCCTCTTA
-----PACKAGING SIGNAL-----
34121 TTCAGTTTTCGCGGAAAATGGCCAAATCTTACTCGGTTACGCCCAAATTTACTACAACA
-----PACKAGING SIGNAL-----
34181 TCCGCCTAAAACCGCGCGAAAATTGTCACTTCCTGTGTACACCGGCGCACACCAAAAACG
-----+
34241 TCACTTTTGCCACATCCGTCGCTTACATGTGTTCCGCCACACTTGCAACATCACACTTCC
34301 GCCACACTACTACGTACCCGCCCCGTTCCACGCCCCGCGCCACGTCACAACTCCACC
+-----ITR-----
34361 CCCTCATTATCATATTGGCTTCAATCCAAAATAAGGTATATTATTGATGATC
-----ITR-----+

Fig. 3C

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1 CATCATCAATAATATACCTTATTTTGGATTGAAGCCAATATGATAATGAGGGGGTGGAGT
----- ITR -----

61 TTGTGACGTGGCGCGGGCGTGGGAACGGGGCGGGTGACGTAGGGCGCGCCGCTAGCGAT
----- ITR ----- ++ --- MCS -----

121 ATCGGATCCCGGTCGACTGAAAATGAGACATATTATCTGCCACGGAGGTGTTATTACCGA
----- E1a -----

181 AGAAATGGCCGCCAGTCTTTTGGACCAGCTGATCGAAGAGGTACTGGCTGATAATCTTCC
----- E1a -----

241 ACCTCCTAGCCATTTTGAACCACCTACCTTTCACGAAGTGTATGATTTAGACGTGACGGC
----- E1a -----

301 CCCCAGAGATCCCAACGAGGAGGCGGTTTCGCAGATTTTCCCGACTCTGTAATGTTGGC
----- E1a -----

361 GGTGCAGGAAGGGATTGACTTACTCACTTTTCCGCCGGCGCCCGGTTCTCCGGAGCCGCC
----- E1a -----

421 TCACCTTTCCCGGCAGCCCGAGCAGCCGGAGCAGAGAGCCTTGGGTCCGGTTTCTATGCC
----- E1a -----

481 AAACCTTGTACCGGAGGTGATCGATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGA
----- E1a -----

541 CGACGAGGATGAAGAGGGTGAGGAGTTTGTGTTAGATTATGTGGAGCACCCCGGCCACGG
----- E1a -----

601 TTGCAGGTCTTGTCATTATCACCGGAGGAATACGGGGGACCCAGATATTATGTGTTTCGCT
----- E1a -----

Fig. 4

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```
1 CATCATCAATAATATACCTTATTTTGGATTGAAGCCAATATGATAATGAGGGGGTGGAGT
+-----ITR-----
61 TTGTGACGTGGCGCGGGGCGTGGGAACGGGGCGGGTGACGTAGGGCGCGATCAAGCTTAT
-----ITR-----+
121 CGATACCGTCGAAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATC
-----polyA-----
181 ACAAATTTACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTC
-----polyA-----
241 ATCAATGTATCTTATCATGTCTGGATCCGCGCCGCTAGCGATATCGGATCCCGGTCGACT
-----+-----
301 GAAAATGAGACATATTATCTGCCACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCT
-----E1a-----
361 TTTGGACCAGCTGATCGAAGAGGTACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGA
-----E1a-----
421 ACCACCTACCCTTCACGAACTGTATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGA
-----E1a-----
481 GGAGGCGGTTTCGCAGATTTTCCCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGA
-----E1a-----
541 CTTACTCACTTTTCCGCCGGCGCCCGGTTCTCCGGAGCCGCCTCACCTTTCCCGGCAGCC
-----E1a-----
601 CGAGCAGCCGGAGCAGAGAGCCTTGGGTCCGGTTTCTATGCCAAACCTTGTACGGGAGGT
-----E1a-----
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Fig. 5

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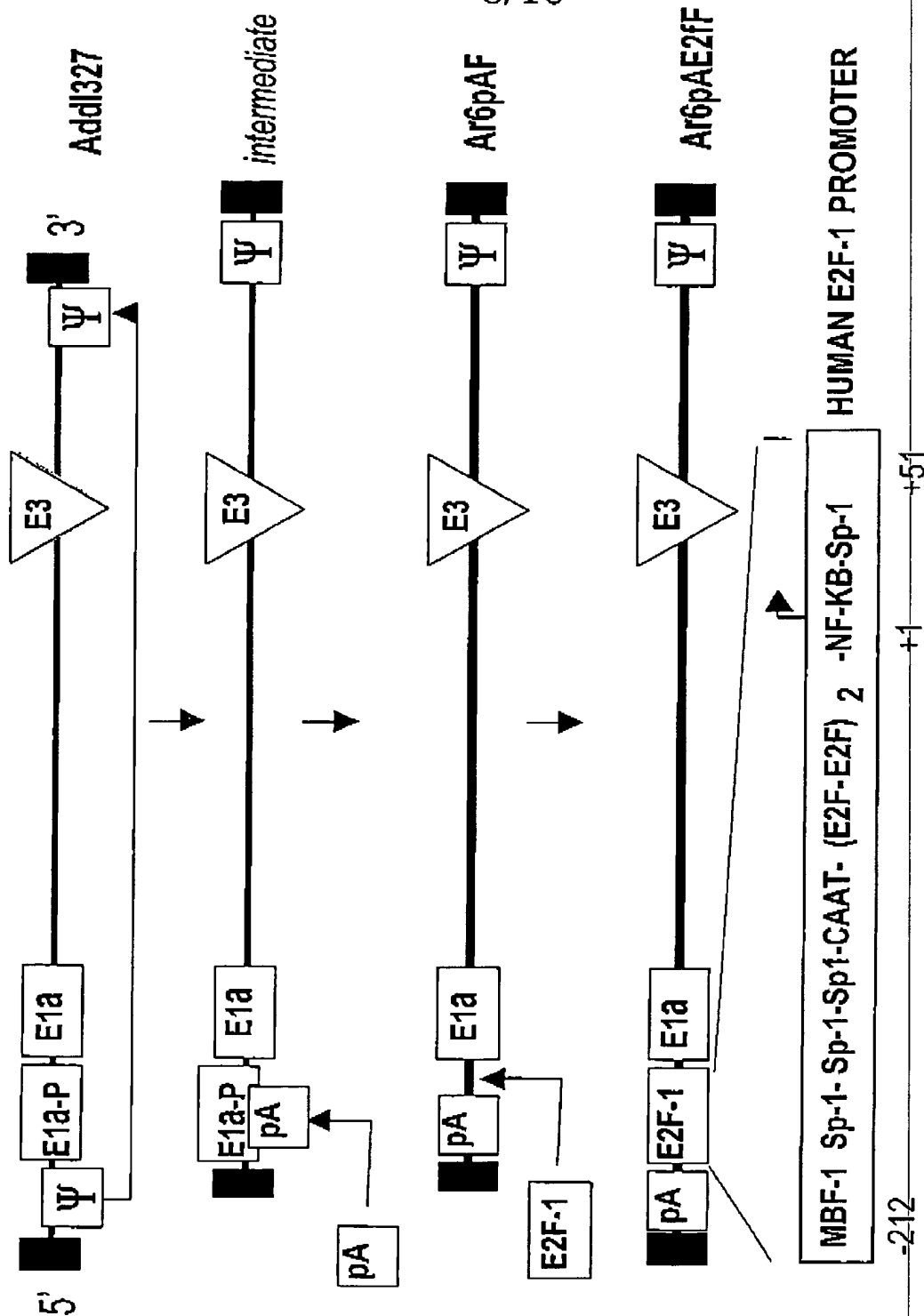


Fig. 6

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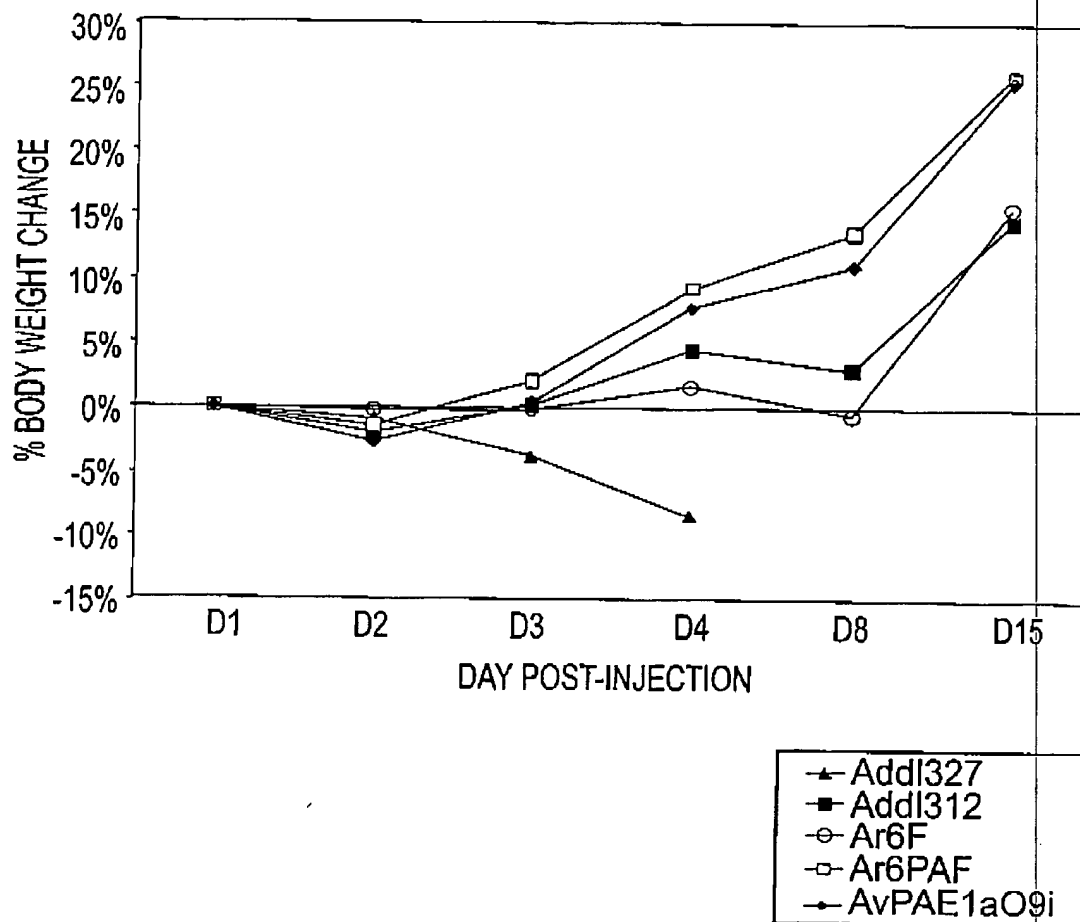


Fig. 7

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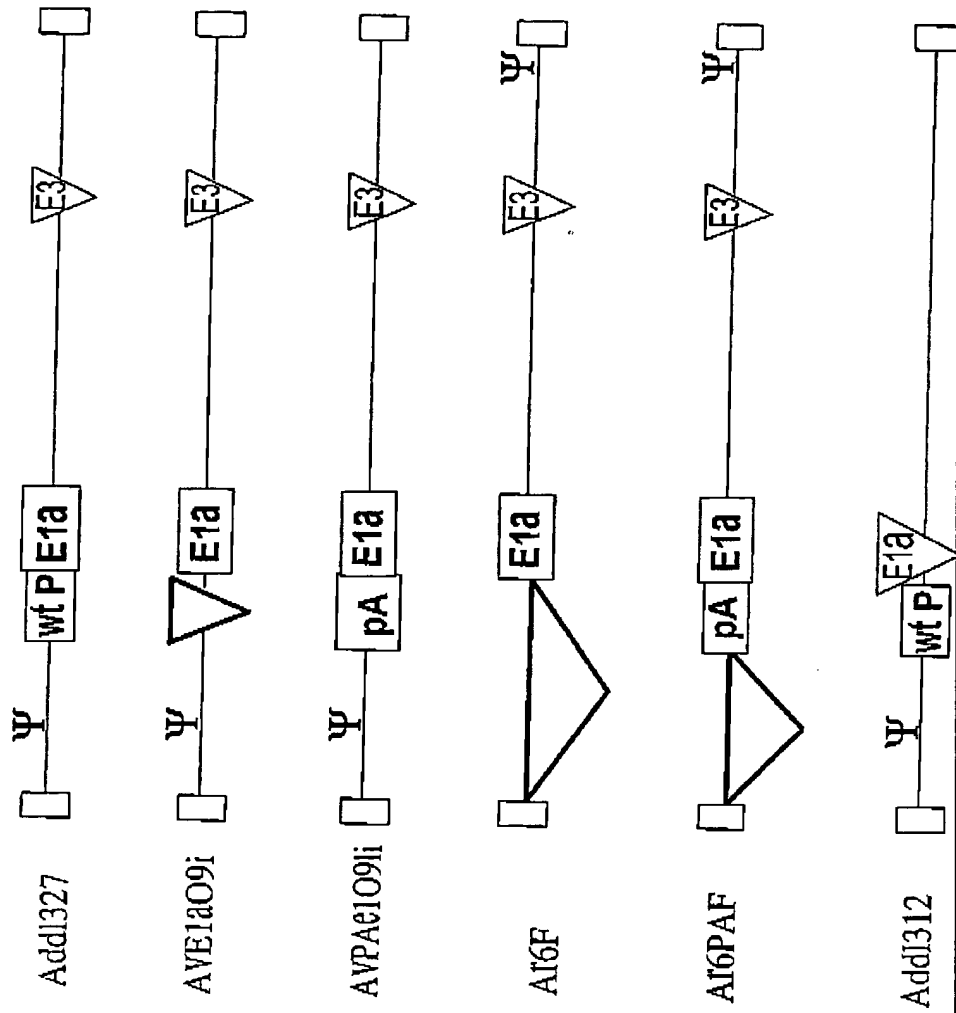


Fig. 8

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